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Defense Date: April 20, 2012

Title: Patterns of genetic structure and gene flow of leopards (*Panthera pardus*) in central India

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## ABSTRACT

Many species currently exist within fragmented habitats much too small for long-term population viability. Landscape fragmentation can have distinct ecological, demographic and genetic consequences. Large mammalian carnivores are particularly vulnerable to habitat loss and fragmentation because of their relatively low numbers, large home ranges, and interactions with humans. However, highly vagile carnivores have the potential to exhibit high rates of dispersal mediated gene flow that may prevent genetic drift and genetic subdivision.

In this study, I standardized laboratory techniques to conduct a genetic study of leopards (*Panthera pardus*) using non-invasively collected samples in order to investigate the genetic structure and patterns of gene flow in central India's Satpura-Maikal landscape. I conducted my study in a 45,000 km<sup>2</sup> area in central India, in five Tiger Reserves: Kanha Tiger Reserve, Satpura Tiger Reserve, Melghat Tiger Reserve, Pench MP (Madhya Pradesh) and Pench Mh (Maharashtra) tiger reserves, and in the forest corridors connecting these reserves. I sampled 15,000 km of forest trails and collected 1,411 felid fecal samples in 2009-2010.

After successfully screening 16 loci using previously published microsatellite primers, I optimized a panel of 7 microsatellites that yields a Probability of Identity between siblings value of  $5.24E-04$ . I used this panel to identify 217 individuals from 287 leopard scats, and identified 101 males and 92 females by amplifying a fragment of the Amelogenin protein gene. I next investigated the genetic structure of leopards in this landscape. Leopards showed high levels of genetic diversity in all sampled populations. Spatial and non-spatial Bayesian analyses revealed at least two admixed genetic populations, contrary to my hypothesis of panmixia. I identified nine individuals as migrants, most of which were in reserves connected by corridors. Genetic differentiation between populations was not explained by geographic distance, and I did not detect any signature of a genetic bottleneck in any of these populations. I then investigated patterns of gene flow in this landscape. I used Bayesian and coalescent-based analyses to estimate contemporary and historical gene flow and found that historical levels of gene flow were significantly higher than levels of contemporary gene flow. Populations with the largest effective population sizes are the largest exporter of migrants at both time scales. The greatest decline in historic versus contemporary gene flow is between pairs of reserves that are currently not connected by corridors.

I conclude that genetic subdivision and discordance in gene flow is due to habitat fragmentation and that existing corridors help to maintain genetic exchange between leopards living in protected areas in central India.